

10/665, 715 9-08-06

GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 8, 2006, 08:30:26 ; Search time 0.1 Seconds
(without alignments)
7.808 Million cell updates/sec

Title: HSBTRCP

Perfect score: 3861

Sequence: 1 TGC GTT GGCT GCG GCCT GGC GTTT GCCAG AAAAAAAA 2151

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2 seqs, 1210 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=soft -Q=y14153.gb_pr -DB=uni.pep -SUFFIX=pto
-OUT=eliz2.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : uni.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

¶

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	3006	77.9	605	1	FBW1A_HUMAN	F-box/WD-repeat pr
2	3006	77.9	605	1	FBW1A_HUMAN	F-box/WD-repeat pr
c 3	57.5	1.5	605	1	FBW1A_HUMAN	F-box/WD-repeat pr
c 4	57.5	1.5	605	1	FBW1A_HUMAN	F-box/WD-repeat pr

ALIGNMENTS

RESULT 1

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RS1kappaB) (pIkappaBalph-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalph-
RT ubiquitin ligase.";
RL Nature 396:590-594(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
RC TISSUE=Lymphoid;
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
RA Thomas D., Strelbel K., Benarous R.;
RT "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu
RT connects CD4 to the ER degradation pathway through an F-box motif.";
RL Mol. Cell 1:565-574(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=99145464; PubMed=9990852;
RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
RL Genes Dev. 13:270-283 (1999).
RN [6]
RP INTERACTION WITH UBQLN1.
RC TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Kedersha N.L., Gill G., Howley P.M.;
RT "The hPLIC proteins may provide a link between the ubiquitination
RT machinery and the proteasome.";
RL Mol. Cell 6:409-419 (2000).
RN [7]
RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RX MEDLINE=22072105; PubMed=12077367;
RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
RL J. Cell Sci. 115:2771-2780 (2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456 (2003).
CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
CC box protein) ubiquitin ligase complex, which mediates the
CC ubiquitination of proteins involved in cell cycle progression,
CC signal transduction and transcription. Regulates the stability of
CC CTNNB1 and participates in Wnt signaling.
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
CC ubiquitination substrates. Binds UBQLN1.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;
 CC IsoId=Q9Y297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y297-2; Sequence=VSP_006764;
 CC -!- SIMILARITY: Contains 1 F-box domain.
 CC -!- SIMILARITY: Contains 7 WD repeats.
 CC
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; AF101784; AAD08702.1; -; mRNA.
 DR EMBL; Y14153; CAA74572.1; -; mRNA.
 DR EMBL; AF129530; AAF04464.1; -; mRNA.
 DR EMBL; BC027994; AAH27994.1; -; mRNA.
 DR PDB; 1P22; X-ray; A=175-605.
 DR IntAct; Q9Y297; -.
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR HGNC; HGNC:1144; BTRC.
 DR MIM; 603482; gene.
 DR LinkHub; Q9Y297; -.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW 3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
 KW Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
 FT CHAIN 1 605 F-box/WD-repeat protein 1A.
 FT FTId=PRO_0000050980.
 FT DOMAIN 190 228 F-box.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
 FT VARSPLIC 17 52 Missing (in isoform 2).
 FT FTId=VSP_006764.
 FT VARIANT 543 543 A -> S (in dbSNP:4151060).
 FT FTId=VAR_022027.
 FT VARIANT 592 592 P -> H (in dbSNP:2270439).
 FT FTId=VAR_020119.
 FT STRAND 176 176
 FT HELIX 180 183
 FT TURN 184 184
 FT HELIX 185 187

FT	TURN	188	188
FT	HELIX	190	197
FT	TURN	198	199
FT	HELIX	202	211
FT	HELIX	213	221
FT	TURN	222	223
FT	HELIX	224	233
FT	TURN	234	234
FT	STRAND	235	235
FT	HELIX	237	244
FT	STRAND	245	247
FT	HELIX	248	251
FT	STRAND	265	265
FT	HELIX	266	285
FT	TURN	286	288
FT	STRAND	296	297
FT	STRAND	301	302
FT	STRAND	306	310
FT	STRAND	313	323
FT	STRAND	325	332
FT	STRAND	335	339
FT	STRAND	343	344
FT	STRAND	346	350
FT	STRAND	353	360
FT	TURN	361	362
FT	STRAND	363	363
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FT	STRAND	375	379
FT	STRAND	384	384
FT	STRAND	386	390
FT	TURN	393	394
FT	STRAND	395	400
FT	TURN	401	402
FT	STRAND	403	403

Alignment Scores:

Pred. No.:	0	Length:	605
Score:	3006.00	Matches:	569
Percent Similarity:	94.0%	Conservative:	0
Best Local Similarity:	94.0%	Mismatches:	0
Query Match:	77.9%	Indels:	36
DB:	1	Gaps:	1

HSBTRCP (1-2151) x FBW1A_HUMAN (1-605)

Qy	70	ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTATG-----	117
Db	1	MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetCysSerMetPro	20
Qy	117	-----	117
Db	21	ArgSerLeuTrpLeuGlyCysSerSerLeuAlaAspSerMetProSerLeuArgCysLeu	40
Qy	118	-----AATTCCTCAGAGAGAGAAGACTGT	141
Db	41	TyrAsnProGlyThrGlyAlaLeuThrAlaPheGlnAsnSerSerGluArgGluAspCys	60

Qy	142	AATAATGGCGAACCCCTAGGAAGATAATACCAAGAGAAGAATTCACTTAGACAGACATAC	201
Db	61	AsnAsnGlyGluProProArgLysIleIleProGluLysAsnSerLeuArgGlnThrTyr	80
Qy	202	AACAGCTGTGCCAGACTCTGCTAAACCAAGAACAGTATGTTAGCAAGCACTGCTATG	261
Db	81	AsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAlaSerThrAlaMet	100
Qy	262	AAGACTGAGAATTGTGTGGCAAAACAAAACATTGCCAATGGCACTTCCAGTATGATTGTG	321
Db	101	LysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSerSerMetIleVal	120
Qy	322	CCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAACTGTGTGTCAAATAC	381
Db	121	ProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeuCysValLysTyr	140
Qy	382	TTTGAGCAGTGGTCAGAGTCAGATCAAGTGGATTGTGGAACATCTTATATCCCAAATG	441
Db	141	PheGluGlnTrpSerGluSerAspGlnValGluPheValGluHisLeuIleSerGlnMet	160
Qy	442	TGTCATTACCAACATGGGCACATAAAACTCGTATCTTAAACCTATGTTGCAGAGAGATTG	501
Db	161	CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe	180
Qy	502	ATAACTGCTCTGCCAGCTCGGGATTGGATCATATCGCTGAGAACATTCTGTACACCTG	561
Db	181	IleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLeu	200
Qy	562	GATGCCAAATCACTATGTGCTGCTGAACCTGTGCAAGGAATGGTACCGAGTGACCTCT	621
Db	201	AspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyrArgValThrSer	220
Qy	622	GATGGCATGCTGTGAAAGAAGCTTATCGAGAGAATGGTCAGGACAGATTCTGTGGAGA	681
Db	221	AspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAspSerLeuTrpArg	240
Qy	682	GGCCTGGCAGAACGAAGAGGATGGGACAGTATTATTCAAAACAAACCTCCTGACGGG	741
Db	241	GlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGly	260
Qy	742	AATGCTCCTCCCAACTCTTTATAGAGCACTTTATCCTAAAATTATAACAAGACATTGAG	801
Db	261	AsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGlu	280
Qy	802	ACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTACAGAGAATTCACTGCCGAAGT	861
Db	281	ThrIleGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSer	300
Qy	862	GAAACAAGCAAAGGAGTTACTGTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTT	921
Db	301	GluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu	320
Qy	922	CGAGACAAACACAATCAAGATCTGGATAAAAACACATTGGAATGCAAGCGAATTCTCACA	981
Db	321	ArgAspAsnThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIleLeuThr	340
Qy	982	GGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGATGAGAGAGTGTACATAACAGGATCA	1041

Db	341	GlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySer	360
Qy	1042	TCGGATTCCACGGTCAGAGTGTGGATGTAATACAGGTGAAATGCTAACACGTTGATT	1101
Db	361	SerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle	380
Qy	1102	CACCATTGTGAAGCAGTTCTGCACCTGCGTTCAATAATGGCATGATGGTACCTGCTCC	1161
Db	381	HisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSer	400
Qy	1162	AAAGATCGTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATTACCTCCGGAGG	1221
Db	401	LysAspArgSerIleAlaValTrpAspMetAlaSerProThrAspIleThrLeuArgArg	420
Qy	1222	GTGCTGGTCGGACACCGAGCTGCTCAATGTTGATGACAAGTACATTGTT	1281
Db	421	ValLeuValGlyHisArgAlaAlaValAsnValValAspPheAspAspLysTyrIleVal	440
Qy	1282	TCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAATTGTAAGG	1341
Db	441	SerAlaSerGlyAspArgThrIleLysValTrpAsnThrSerThrCysGluPheValArg	460
Qy	1342	ACCTTAAATGGACACAAACGAGGCATTGCCTGTTGCAGTACAGGGACAGGGCTGGTAGTG	1401
Db	461	ThrLeuAsnGlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAspArgLeuValVal	480
Qy	1402	AGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAACATGTTGTCATGTTACGA	1461
Db	481	SerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGlyAlaCysLeuArg	500
Qy	1462	GTGTTAGAAGGCCATGAGGAATTGGTGCCTGTATTGATAACAAGAGGGATAGTC	1521
Db	501	ValLeuGluGlyHisGluLeuValArgCysIleArgPheAspAsnLysArgIleVal	520
Qy	1522	AGTGGGGCTATGATGGAAAAATTAAAGTGTGGATCTTGTGGCTGCTTGGACCCCCGT	1581
Db	521	SerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAlaLeuAspProArg	540
Qy	1582	GCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGCATTCCGGAAGAGTTTCGA	1641
Db	541	AlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheArg	560
Qy	1642	CTACAGTTGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACAATCCTCATCTGG	1701
Db	561	LeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThrIleLeuIleTrp	580
Qy	1702	GACTTCCTAAATGATCCAGCTGCCAAGCTGAACCCCCCGTTCCCTCTCGAACATAC	1761
Db	581	AspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerProSerArgThrTyr	600
Qy	1762	ACCTACATCTCCAGA	1776
Db	601	ThrTyrIleSerArg	605

RESULT 2

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RS1kappaB) (pIkappaBalphalpha-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RX MEDLINE=22072105; PubMed=12077367;
RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
RL J. Cell Sci. 115:2771-2780 (2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456 (2003).
CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
CC box protein) ubiquitin ligase complex, which mediates the
CC ubiquitination of proteins involved in cell cycle progression,
CC signal transduction and transcription. Regulates the stability of
CC CTNNB1 and participates in Wnt signaling.
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
CC ubiquitination substrates. Binds UBQLN1.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y297-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Y297-2; Sequence=VSP_006764;
CC -!- SIMILARITY: Contains 1 F-box domain.

CC -!- SIMILARITY: Contains 7 WD repeats.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
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 DR EMBL; AF101784; AAD08702.1; -; mRNA.
 DR EMBL; Y14153; CAA74572.1; -; mRNA.
 DR EMBL; AF129530; AAF04464.1; -; mRNA.
 DR EMBL; BC027994; AAH27994.1; -; mRNA.
 DR PDB; 1P22; X-ray; A=175-605.
 DR IntAct; Q9Y297; -.
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR HGNC; HGNC:1144; BTRC.
 DR MIM; 603482; gene.
 DR LinkHub; Q9Y297; -.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
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 KW 3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
 KW Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
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 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
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 FT VARSPLIC 17 52 Missing (in isoform 2).
 FT /FTId=VSP_006764.
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 FT /FTId=VAR_022027.
 FT VARIANT 592 592 P -> H (in dbSNP:2270439).
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 FT HELIX 213 221

FT	TURN	222	223
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Alignment Scores:

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Percent Similarity:	94.0%	Conservative:	0
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Query Match:	77.9%	Indels:	36
DB:	1	Gaps:	1

HSBTRCP (1-2151) x FBW1A_HUMAN (1-605)

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Qy	118	-----AATTCTCAGAGAGAGAAGACTGT	141
Db	41	TyrAsnProGlyThrGlyAlaLeuThrAlaPheGlnAsnSerSerGluArgGluAspCys	60
Qy	142	AATAATGGCGAACCCCTAGGAAGATAATACCAAGAGAAGAATTCACTTAGACAGACATAC	201
Db	61	AsnAsnGlyGluProProArgLysIleIleProGluLysAsnSerLeuArgGlnThrTyr	80
Qy	202	AACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTAGCAAGCACTGCTATG	261

Db	81	AsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAlaSerThrAlaMet	100
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Qy	502	ATAACTGCTCTGCCAGCTCGGGATTGGATCATATCGCTGAGAACATTCTGTACACCTG	561
Db	181	IleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLeu	200
Qy	562	GATGCCAAATCACTATGTGCTGCTGAACATTGTGTGCAAGGAATGGTACCGAGTGACCTCT	621
Db	201	AspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyrArgValThrSer	220
Qy	622	GATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGGACAGATTCTGTGGAGA	681
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Qy	682	GGCCTGGCAGAACGAAAGAGGATGGGGACAGTATTATTCAAAACAAACCTGACGGG	741
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Qy	802	ACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTACAGAGAATTCACTGCCGAAGT	861
Db	281	ThrIleGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSer	300
Qy	862	GAAACAAGCAAAGGAGTTACTGTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTT	921
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Qy	922	CGAGACAACACAATCAAGATCTGGATAAAAACACATTGGAATGCAAGCGAATTCTCACA	981
Db	321	ArgAspAsnThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIleLeuThr	340
Qy	982	GGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCA	1041
Db	341	GlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySer	360
Qy	1042	TCGGATTCCACGGTCAGAGTGTGGGATGTAACAGGTGAAATGCTAACACGTTGATT	1101

Db 361 SerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle 380

Qy 1102 CACCATTGTGAAGCAGTTCTGCACCGCTTCAATAATGGCATGATGGTGACCTGCTCC 1161
 |||||||
 Db 381 HisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSer 400

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Qy 1402 AGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTACGA 1461
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 Db 481 SerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGlyAlaCysLeuArg 500

Qy 1462 GTGTTAGAAGGCCATGAGGAATTGGTGCCTGTATTGATTTGATAACAAGAGGGATAGTC 1521
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 Db 501 ValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsnLysArgIleVal 520

Qy 1522 AGTGGGGCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCTTGGACCCCGT 1581
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 Db 521 SerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAlaLeuAspProArg 540

Qy 1582 GCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGCATTCCGGAAAGAGTTTCTGA 1641
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 Db 541 AlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheArg 560

Qy 1642 CTACAGTTGATGAATTCCAGATTGTCAGTAGTCACATGATGACACAATCCTCATCTGG 1701
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 Db 561 LeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThrIleLeuIleTrp 580

Qy 1702 GACTTCCTAAATGATCCAGCTGCCAAGCTGAACCCCCCGTTCCCTCTCGAACATAC 1761
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RESULT 3

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.

AC Q9Y297; Q9Y213;

DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1999, sequence version 1.

DT 07-FEB-2006, entry version 52.

DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RS1kappaB) (pIkappaBalph-a-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalph-a-
RT ubiquitin ligase.";
RL Nature 396:590-594(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
RC TISSUE=Lymphoid;
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
RA Thomas D., Strelbel K., Benarous R.;
RT "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu
RT connects CD4 to the ER degradation pathway through an F-box motif.";
RL Mol. Cell 1:565-574(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]

RP CHARACTERIZATION.
RX MEDLINE=99145464; PubMed=9990852;
RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
RL Genes Dev. 13:270-283 (1999).
RN [6]
RP INTERACTION WITH UBQLN1.
RC TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Kedersha N.L., Gill G., Howley P.M.;
RT "The hPLIC proteins may provide a link between the ubiquitination
RT machinery and the proteasome.";
RL Mol. Cell 6:409-419 (2000).
RN [7]
RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RX MEDLINE=22072105; PubMed=12077367;
RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
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RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456 (2003).
CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
CC box protein) ubiquitin ligase complex, which mediates the
CC ubiquitination of proteins involved in cell cycle progression,
CC signal transduction and transcription. Regulates the stability of
CC CTNNB1 and participates in Wnt signaling.
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
CC ubiquitination substrates. Binds UBQLN1.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y297-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Y297-2; Sequence=VSP_006764;
CC -!- SIMILARITY: Contains 1 F-box domain.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----

DR EMBL; AF101784; AAD08702.1; -; mRNA.
 DR EMBL; Y14153; CAA74572.1; -; mRNA.
 DR EMBL; AF129530; AAF04464.1; -; mRNA.
 DR EMBL; BC027994; AAH27994.1; -; mRNA.
 DR PDB; 1P22; X-ray; A=175-605.
 DR IntAct; Q9Y297; -.
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR HGNC; HGNC:1144; BTRC.
 DR MIM; 603482; gene.
 DR LinkHub; Q9Y297; -.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW 3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
 KW Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
 FT CHAIN 1 605 F-box/WD-repeat protein 1A.
 FT /FTId=PRO_0000050980.
 FT DOMAIN 190 228 F-box.
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 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
 FT VARSPLIC 17 52 Missing (in isoform 2).
 FT /FTId=VSP_006764.
 FT VARIANT 543 543 A -> S (in dbSNP:4151060).
 FT /FTId=VAR_022027.
 FT VARIANT 592 592 P -> H (in dbSNP:2270439).
 FT /FTId=VAR_020119.
 FT STRAND 176 176
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 FT STRAND 235 235
 FT HELIX 237 244

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FT	HELIX	248	251
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FT	TURN	393	394
FT	STRAND	395	400
FT	TURN	401	402
FT	STRAND	403	403

Alignment Scores:

Pred. No.:	0	Length:	605
Score:	57.50	Matches:	28
Percent Similarity:	37.3%	Conservative:	13
Best Local Similarity:	25.5%	Mismatches:	60
Query Match:	1.5%	Indels:	9
DB:	1	Gaps:	3

HSBTRCP (1-2151) x FBW1A HUMAN (1-605)

Qy	1238	CGGTGTCCGACCAGCACCCTCGGAGGGTAATGTCAGTTGGGAGGCCATATCCCATACA	1179
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Qy	1178	GCAATGGAACGATCTTGGAGCAGGTACCATCATGCCATTATTGAAACGCAAGTGCAGA	1119
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Db	307	TyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu-----ArgAspAsn	323
Qy	1118	ACTGCTTCACAATGGTGAATCAACGTGTTAGCATTACCTGTATTTACATCCCACACT	1059
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Db	344	GlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySerSer-----	361
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Qy	947	TCCCCAGATCTTGATTGTGTTGTCGAAGG	918

Db 381 HisHisCysGluAlaValLeuHisLeuArg 390

RESULT 4

FBW1A_HUMAN

ID FBW1A_HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RS1kappaB) (pIkappaBalph-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalph-
RT ubiquitin ligase.";
RL Nature 396:590-594 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
RC TISSUE=Lymphoid;
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
RA Thomas D., Strelbel K., Benarous R.;
RT "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu
RT connects CD4 to the ER degradation pathway through an F-box motif.";
RL Mol. Cell 1:565-574 (1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=99145464; PubMed=9990852;
RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
RL Genes Dev. 13:270-283 (1999).
RN [6]
RP INTERACTION WITH UBQLN1.
RC TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Kedersha N.L., Gill G., Howley P.M.;
RT "The hPLIC proteins may provide a link between the ubiquitination
RT machinery and the proteasome.";
RL Mol. Cell 6:409-419 (2000).
RN [7]
RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RX MEDLINE=22072105; PubMed=12077367;
RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
RL J. Cell Sci. 115:2771-2780 (2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456 (2003).
CC -!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
CC box protein) ubiquitin ligase complex, which mediates the
CC ubiquitination of proteins involved in cell cycle progression,
CC signal transduction and transcription. Regulates the stability of
CC CTNNB1 and participates in Wnt signaling.
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
CC ubiquitination substrates. Binds UBQLN1.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;

CC IsoId=Q9Y297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y297-2; Sequence=VSP_006764;
 CC -!- SIMILARITY: Contains 1 F-box domain.
 CC -!- SIMILARITY: Contains 7 WD repeats.
 CC -----
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 CC -----
 DR EMBL; AF101784; AAD08702.1; -; mRNA.
 DR EMBL; Y14153; CAA74572.1; -; mRNA.
 DR EMBL; AF129530; AAF04464.1; -; mRNA.
 DR EMBL; BC027994; AAH27994.1; -; mRNA.
 DR PDB; 1P22; X-ray; A=175-605.
 DR IntAct; Q9Y297; -.
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR HGNC; HGNC:1144; BTRC.
 DR MIM; 603482; gene.
 DR LinkHub; Q9Y297; -.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW 3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
 KW Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
 FT CHAIN 1 605 F-box/WD-repeat protein 1A.
 FT DOMAIN 190 228 F-box.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
 FT VARSPLIC 17 52 Missing (in isoform 2).
 FT /FTId=VSP_006764.
 FT VARIANT 543 543 A -> S (in dbSNP:4151060).
 FT /FTId=VAR_022027.
 FT VARIANT 592 592 P -> H (in dbSNP:2270439).
 FT /FTId=VAR_020119.
 FT STRAND 176 176
 FT HELIX 180 183
 FT TURN 184 184
 FT HELIX 185 187
 FT TURN 188 188

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FT	TURN	198	199
FT	HELIX	202	211
FT	HELIX	213	221
FT	TURN	222	223
FT	HELIX	224	233
FT	TURN	234	234
FT	STRAND	235	235
FT	HELIX	237	244
FT	STRAND	245	247
FT	HELIX	248	251
FT	STRAND	265	265
FT	HELIX	266	285
FT	TURN	286	288
FT	STRAND	296	297
FT	STRAND	301	302
FT	STRAND	306	310
FT	STRAND	313	323
FT	STRAND	325	332
FT	STRAND	335	339
FT	STRAND	343	344
FT	STRAND	346	350
FT	STRAND	353	360
FT	TURN	361	362
FT	STRAND	363	363
FT	STRAND	365	372
FT	STRAND	375	379
FT	STRAND	384	384
FT	STRAND	386	390
FT	TURN	393	394
FT	STRAND	395	400
FT	TURN	401	402
FT	STRAND	403	403

Alignment Scores:

Pred. No.:	0	Length:	605
Score:	57.50	Matches:	28
Percent Similarity:	37.3%	Conservative:	13
Best Local Similarity:	25.5%	Mismatches:	60
Query Match:	1.5%	Indels:	9
DB:	1	Gaps:	3

HSBTRCP (1-2151) x FBW1A_HUMAN (1-605)

Qy	1238 CGGTGTCCGACCAGCACCCCTCCGGAGGGTAATGTCAGTTGGGGAGGCCATATCCATACA	1179
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Db	287 ArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSerGluThrSerLysGlyVal	306
Qy	1178 GCAATGGAACGATCTTGGAGCAGGTACCATCATGCCATTATTGAAACGCAAGTGCAGA	1119
	::: :::: :::: :::: ::::	
Db	307 TyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu-----ArgAspAsn	323
Qy	1118 ACTGCTTCACAATGGTGAATCAACGTGTTAGCATTACCTGTATTACATCCCACACT	1059
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Db	324 ThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIleLeuThrGlyHisThr	343
Qy	1058 -----CTGACCGTGGAAATCCGATGATCCTGTTATGATCACTCTCTCATCATACTGG	1008

Db	344 GlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySerSer-----	361
Qy	1007 AGACAGAGGACTAACCTGTATGGCCTGTGAGAATTGCTTGCATTCCAATGTGTTTTA	948
Db	362 ---AspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle	380
Qy	947 TCCCAGATCTTGATTGTGTTCTCGAAGG	918
Db	381 HisHisCysGluAlaValLeuHisLeuArg	390

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